

SEQUENCE LISTING

<110> Sticklen, Masomeh B
 Maqbool, Shahina B
 Dale, Bruce E

<120> TRANSGENIC PLANTS CONTAINING LIGNINASE AND CELLULASE WHICH
 DEGRADE
 LIGNIN AND CELLULOSE TO FERMENTABLE SUGARS

<130> MSU 4.1-539

<150> 60/242,408

<151> 2000-10-20

<160> 19

<170> PatentIn version 3.1

<210> 1

<211> 1110

<212> DNA

<213> Oryza sativa

<400> 1

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1110

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Val Pro Arg Ala	
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Thr Ile Arg Leu Pro Tyr Ser Asp Asp Ile Leu Lys Pro Gly Thr Met	
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tcg gcg ctg tgg tac acg agc agc gtc tcg gag gct acg tgg att tcc	1363
Ser Ala Leu Trp Tyr Thr Ser Ser Val Ser Glu Ala Thr Trp Ile Ser	
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Asp Leu Gln Ala Leu Ala Gln Arg Tyr Lys Gly Asn Pro Thr Val Val	
185 190 195	

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Gly Phe Asp Leu His Asn Glu Pro His Asp Pro Ala Cys Trp Gly Cys	
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Gly Asp Pro Ser Ile Asp Trp Arg Leu Ala Ala Glu Arg Ala Gly Asn	
215 220 225	
gcc gtg ctc tcg gtg aat ccg aac ctg ctc att ttc gtc gaa ggt gtg	1555
Ala Val Leu Ser Val Asn Pro Asn Leu Leu Ile Phe Val Glu Gly Val	
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Gln Ser Tyr Asn Gly Asp Ser Tyr Trp Trp Gly Gly Asn Leu Gln Gly	
245 250 255 260	
gcc gcc cag tac ccg gtc gtg ctg aac gtg ccg aac cgc ctg gtg tac	1651
Ala Gly Gln Tyr Pro Val Val Leu Asn Val Pro Asn Arg Leu Val Tyr	
265 270 275	
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Ser Ala His Asp Tyr Ala Thr Ser Val Tyr Pro Gln Thr Trp Phe Ser	
280 285 290	
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Asp Pro Thr Phe Pro Asn Asn Met Pro Gly Ile Trp Asn Lys Asn Trp	
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Gly Tyr Leu Phe Asn Gln Asn Ile Ala Pro Val Trp Leu Gly Glu Phe	
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Val Gln Tyr Leu Arg Pro Thr Ala Gln Tyr Gly Ala Asp Ser Phe Gln	
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Trp Thr Phe Trp Ser Trp Asn Pro Asp Ser Gly Asp Thr Gly Gly Ile	
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375 380 385	
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ccg acg cca acg ctg acc cct act gct acg ccc acg ccc acg gca agc	2179
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Tyr Gln Val Asn Ser Asp Trp Gly Asn Gly Phe Thr Val Thr Val Ala	
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Val Ile Gln Pro Gly Gln Asn Thr Thr Phe Gly Phe Gln Ala Ser Tyr	
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Thr Gly Ser Asn Ala Ala Pro Thr Val Ala Cys Ala Ala Ser	
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Gly Leu Trp Ser Arg Asp Tyr Arg Ser Met Leu Asp Gln Ile Lys Ser
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Leu Gly Tyr Asn Thr Ile Arg Leu Pro Tyr Ser Asp Asp Ile Leu Lys
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Pro Gly Thr Met Pro Asn Ser Ile Asn Phe Tyr Gln Met Asn Gln Asp
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Ala Gly Gln Ile Gly Leu Arg Ile Ile Leu Asp Arg His Arg Pro Asp
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Cys Ser Gly Gln Ser Ala Leu Trp Tyr Thr Ser Ser Val Ser Glu Ala
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Thr Trp Ile Ser Asp Leu Gln Ala Leu Ala Gln Arg Tyr Lys Gly Asn
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Pro Thr Val Val Gly Phe Asp Leu His Asn Glu Pro His Asp Pro Ala
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Cys Trp Gly Cys Gly Asp Pro Ser Ile Asp Trp Arg Leu Ala Ala Glu
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Arg Ala Gly Asn Ala Val Leu Ser Val Asn Pro Asn Leu Leu Ile Phe
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Val Glu Gly Val Gln Ser Tyr Asn Gly Asp Ser Tyr Trp Trp Gly Gly
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Asn Leu Gln Gly Ala Gly Gln Tyr Pro Val Val Leu Asn Val Pro Asn
 260 265 270

Arg Leu Val Tyr Ser Ala His Asp Tyr Ala Thr Ser Val Tyr Pro Gln
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Thr Trp Phe Ser Asp Pro Thr Phe Pro Asn Asn Met Pro Gly Ile Trp
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Asn Lys Asn Trp Gly Tyr Leu Phe Asn Gln Asn Ile Ala Pro Val Trp
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Leu Gly Glu Phe Gly Thr Thr Leu Gln Ser Thr Thr Asp Gln Thr Trp
325 330 335

Leu Lys Thr Leu Val Gln Tyr Leu Arg Pro Thr Ala Gln Tyr Gly Ala
340 345 350

Asp Ser Phe Gln Trp Thr Phe Trp Ser Trp Asn Pro Asp Ser Gly Asp
355 360 365

Thr Gly Gly Ile Leu Lys Asp Asp Trp Gln Thr Val Asp Thr Val Lys
370 375 380

Asp Gly Tyr Leu Ala Pro Ile Lys Ser Ser Ile Phe Asp Pro Val Gly
385 390 395 400

Ala Ser Ala Ser Pro Ser Ser Gln Pro Ser Pro Ser Val Ser Pro Ser
405 410 415

Pro Ser Pro Ser Pro Ser Ala Ser Arg Thr Pro Thr Pro Thr Pro Thr
420 425 430

Pro Thr Ala Ser Pro Thr Pro Thr Leu Thr Pro Thr Ala Thr Pro Thr
435 440 445

Pro Thr Ala Ser Pro Thr Pro Ser Pro Thr Ala Ala Ser Gly Ala Arg
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Cys Thr Ala Ser Tyr Gln Val Asn Ser Asp Trp Gly Asn Gly Phe Thr
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Val Thr Val Ala Val Thr Asn Ser Gly Ser Val Ala Thr Lys Thr Trp
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Thr Val Ser Trp Thr Phe Gly Gly Asn Gln Thr Ile Thr Asn Ser Trp
500 505 510

Asn Ala Ala Val Thr Gln Asn Gly Gln Ser Val Thr Ala Arg Asn Met
515 520 525

Ser Tyr Asn Asn Val Ile Gln Pro Gly Gln Asn Thr Thr Phe Gly Phe
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Gln Ala Ser Tyr Thr Gly Ser Asn Ala Ala Pro Thr Val Ala Cys Ala
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Ala Ser

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Tyr Asn Glu Asp Gly Lys Gly Leu Ser Val Gln Asp Val Met Pro Arg	
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Ala Arg Gly Asp Arg Pro Ser Thr Thr Ala Tyr Ala Glu Asp Ile Ser	
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Ser Arg Ile Phe Pro Leu Gly Asp Glu Thr Glu Pro Asn Glu Glu Gly	
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 35 40 45

Gly Ile Met Ala His Pro Thr Gln Ala Pro Thr Pro Asp Asn Leu Gln
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Ala Arg Gly Asp Arg Pro Ser Thr Thr Ala Tyr Ala Glu Asp Ile Ser
 65 70 75 80

Leu Phe Ala Glu Met Gly Phe Lys Val Phe Arg Phe Ser Ile Ala Trp
 85 90 95

Ser Arg Ile Phe Pro Leu Gly Asp Glu Thr Glu Pro Asn Glu Glu Gly
 100 105 110

Xaa Ala Phe Tyr Asp Arg Val Leu Asp Glu Leu Glu Lys His Gly Ile
 115 120 125

Glu Pro Leu Val Thr Ile Ser His Tyr Glu Thr Pro Leu His Leu Ala
 130 135 140

Arg Thr Tyr Xaa Gly Trp Thr Asp Arg Arg Leu Ile Gly Phe Phe Glu
 145 150 155 160

Arg Tyr Ala Arg Thr Leu Phe Glu Arg Tyr Gly Lys Arg Val Lys Tyr
 165 170 175

Trp Leu Thr Phe Asn Glu Ile Asn Ser Val Leu His Glu Pro Phe Leu
 180 185 190

Ser Gly Gly Val Ala Thr Pro Lys Asp Arg Pro Pro Glu Gln Asp Leu
 195 200 205

Tyr Gln Ala Ile Gln Asn Glu Leu Val Ala Ser Ala Ala Ala Thr Arg
 210 215 220

Ile Ala His Glu Thr Asn Pro Asp Ile Gln Val Gly Cys Met Ile Leu
 225 230 235 240

Ala Asp Pro Thr Tyr Pro Leu Thr Pro Asp Pro Arg Asp Val Trp Ala
245 250 255

Ala Lys Gln Ala Glu Arg Ala Asn Tyr Ala Phe Gly Asp Leu His Val
260 265 270

Arg Gly Glu Tyr Pro Gly Tyr Leu Arg Arg Thr Leu Arg Asp Lys Gly
275 280 285

Ile Glu Leu Glu Ile Thr Glu Glu Asp Arg Val Leu Leu Arg Glu His
290 295 300

Thr Val Asp Phe Val Ser Phe Ser Tyr Tyr Met Xaa Val Cys Glu Thr
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Val Thr Gln Ser Ala Glu Ala Gly Arg Gly Asn Leu Met Gly Gly Val
325 330 335

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340 345 350

Ala Gly Leu Arg Thr Ile Leu Asn Asp Tyr Trp Asp Arg Trp Gly Lys
355 360 365

Pro Leu Phe Ile Val Glu Asn Gly Leu Gly Ala Lys Asp Val Leu Val
370 375 380

Asp Gly Pro Asn Gly Pro Thr Val Glu Asp Asp Tyr Arg Ile Ala Tyr
385 390 395 400

Met Asn Asp His Leu Val Gln Val Ala Glu Ala Ile Ala Asp Gly Val
405 410 415

Glu Val Leu Gly Tyr Thr Ser Trp Gly Cys Ile Asp Leu Val Ser Ala
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Ser Thr Ala Gln Met Ser Lys Arg Tyr Gly Phe Ile Tyr Val Asp Arg
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Asp Asp Gly Gly Asn Gly Thr Leu Ala Arg Tyr Arg Lys Lys Ser Phe
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 <213> Streptococcus salivarius

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caa cat gct tca gaa att atc ggt caa gat aac gtt gac ctt acg cta      460
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gcg gca gga gct tca gcc aag gtt tca aac ttg aca gta gcg tca gag      508
Ala Ala Gly Ala Ser Ala Lys Val Ser Asn Leu Thr Val Ala Ser Glu
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Trp Leu Thr Asn Asn Thr Gly Tyr Leu Val Thr Ile Ser Val Asn Asp
40               45               50               55

aaa tca ggc aat gtc ttg tca agc aag cgc gct ggc ttg tct gtt gaa      604
Lys Ser Gly Asn Val Leu Ser Ser Lys Arg Ala Gly Leu Ser Val Glu
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gat gat tgg aca gtt ttc cca cgt tac ggt atc gta gca ggt tca cca      652
Asp Asp Trp Thr Val Phe Pro Arg Tyr Gly Ile Val Ala Gly Ser Pro
75               80               85

act gat caa aac agt att ctt gtt aaa aat ctt gaa gcc tac cgt aaa      700
Thr Asp Gln Asn Ser Ile Leu Val Lys Asn Leu Glu Ala Tyr Arg Lys
90               95               100

gag ctt gag ctc atg aag tct atg aat atc aac tca tat ttc ttc tat      748
Glu Leu Glu Leu Met Lys Ser Met Asn Ile Asn Ser Tyr Phe Phe Tyr
105               110               115

gat gct tat aat gaa gct aca gat cct ttc cca gaa ggt gtc gat agc      796
Asp Ala Tyr Asn Glu Ala Thr Asp Pro Phe Pro Glu Gly Val Asp Ser
120               125               130               135

ttt gtt caa aaa tgg aat acc tgg agt cac act cag gtt gac act aag      844
Phe Val Gln Lys Trp Asn Thr Trp Ser His Thr Gln Val Asp Thr Lys
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170 175 180	
ctt cca ctt gct gct ttg gct tat aac ttc tac gat agc ttt ggt aag Leu Pro Leu Ala Ala Leu Ala Tyr Asn Phe Tyr Asp Ser Phe Gly Lys	988
185 190 195	
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395 400 405	

Asn Leu Thr Val Ala Ser Glu Trp Leu Thr Asn Asn Thr Gly Tyr Leu
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 His Thr Gln Val Asp Thr Lys Ala Val Lys Glu Leu Val Asp Gln Val
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 His Lys Ser Gly Ala Val Ala Met Leu Tyr Asn Met Ile Ser Ala Asp
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 Gln Lys Tyr Ile Ala Gly Val Met Lys Ser Ala Met Asp Arg Met Gly
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 Phe Asp Gly Trp Gln Gly Asp Thr Ile Gly Asp Asn Arg Val Thr Asp
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Lys Tyr Tyr Ile Thr Ile Asn Asp Val Asn Gly Gly Asn Asp Asp Lys
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Leu Ala Lys Ala Arg Gln Asp Val Val Tyr Asn Glu Leu Trp Thr Asn
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Gly Gly Tyr His Met Ser Ile Ala Ala Leu Ala Asn Ala Asn Ala Ala
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Leu Gly Val Thr Gly Asp Gln Val Trp Thr Phe Ala Lys Ser Gly Lys
 485 490 495

Gly Phe Ser Thr Val Gln Met Ile Asn Met Met Gly Ile Asn Ala Gly
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Trp His Asn Glu Glu Gly Tyr Ala Asp Asn Lys Thr Pro Asp Ala Gln
 515 520 525

Glu Asn Leu Thr Val Arg Leu Ser Leu Ala Gly Lys Thr Ala Gln Glu
 530 535 540

Ala Ala Lys Ile Ala Asp Gln Val Tyr Val Thr Ser Pro Asp Asp Trp
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Ala Thr Ser Ser Met Lys Lys Ala Gln Ala Ser Leu Glu Thr Asp Glu
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Asn Gly Gln Pro Val Leu Val Ile Ser Val Pro Lys Leu Thr Leu Trp
580 585 590

Asn Met Leu Tyr Ile Lys Glu Asp Thr Thr Ala Thr Pro Val Glu Pro
595 600 605

Val Thr Asn Gln Ala Gly Lys Lys Val Asp Asn Thr Val Thr Ser Glu
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Asp Gly Val His Thr Ala Ser Asn Ala Ala Cys Cys Ala Trp Phe Pro
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Val Leu Asp Asp Ile Gln Gln Asn Leu Phe His Gly Gly Gln Cys Gly
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Ala Glu Ala His Glu Ala Leu Arg Met Val Phe His Asp Ser Ile Ala
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Ile Ser Pro Lys Leu Gln Ser Gln Gly Lys Phe Gly Gly Gly Gly Ala
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Asp Gly Ser Ile Ile Thr Phe Ser Ser Ile Glu Thr Thr Tyr His Pro
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Asn Ile Gly Leu Asp Glu Val Val Ala Ile Gln Lys Pro Phe Ile Ala
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Lys His Gly Val Thr Arg Gly Asp Phe Ile Ala Phe Ala Gly Ala Val
 130 135 140

Gly Val Ser Asn Cys Pro Gly Ala Pro Gln Met Gln Phe Phe Leu Gly
 145 150 155 160

Arg Pro Glu Ala Thr Gln Ala Ala Pro Asp Gly Leu Val Pro Glu Pro
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Phe His Thr Ile Asp Gln Val Leu Ala Arg Met Leu Asp Ala Gly Gly

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54

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Phe Ser Phe Phe Pro Pro Gly Met Thr Met Asp Asp Val Glu Gln Ala			
	330	335	340
tgc gcc gag acg ccc ttc ccg act ctc tcg act ctc cct ggc ccc gcg			1110
Cys Ala Glu Thr Pro Phe Pro Thr Leu Ser Thr Leu Pro Gly Pro Ala			
	345	350	355
acc tcc gtc gct cgc atc cct cct cct cct ggt gct taa gcagccatca			1159
Thr Ser Val Ala Arg Ile Pro Pro Pro Gly Ala			
	365	370	
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tcgtcg			1285
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<213>	Phanerochaete chrysosporium		
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Arg Ala Ala Gln Gly Ala Ala Val Glu Lys Arg Ala Thr Cys Ser Asn			
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Gly Lys Val Val Pro Ala Ala Ser Cys Cys Thr Trp Phe Asn Val Leu			
	35	40	45
Ser Asp Ile Gln Glu Asn Leu Phe Asn Gly Gly Gln Cys Gly Ala Glu			
	50	55	60
Ala His Glu Ser Ile Arg Leu Val Phe His Asp Ala Ile Ala Ile Ser			
65	70	75	80

Pro Ala Met Glu Pro Gln Ala Ser Ser Val Arg Gly Ala Asp Gly Ser
 85 90 95

Ile Met Ile Phe Asp Glu Ile Glu Thr Asn Phe His Pro Asn Ile Gly
 100 105 110

Leu Asp Glu Ile Val Arg Leu Gln Lys Pro Phe Val Gln Lys His Gly
 115 120 125

Val Thr Pro Gly Asp Phe Ile Ala Phe Ala Gly Ala Val Ala Leu Ser
 130 135 140

Asn Cys Pro Gly Ala Pro Gln Met Asn Phe Phe Thr Gly Arg Ala Pro
 145 150 155 160

Ala Thr Gln Pro Ala Pro Asp Gly Leu Val Pro Glu Pro Phe His Ser
 165 170 175

Val Asp Gln Ile Ile Asp Arg Val Phe Asp Ala Gly Glu Phe Asp Glu
 180 185 190

Leu Glu Leu Val Trp Met Leu Ser Ala His Ser Val Ala Ala Ala Asn
 195 200 205

Asp Ile Asp Pro Asn Ile Gln Gly Leu Pro Phe Asp Ser Thr Pro Gly
 210 215 220

Ile Phe Asp Ser Gln Phe Phe Val Glu Thr Gln Leu Ala Gly Thr Gly
 225 230 235 240

Phe Thr Gly Gly Ser Asn Asn Gln Gly Glu Val Ser Ser Pro Leu Pro
 245 250 255

Gly Glu Met Arg Leu Gln Ser Asp Phe Leu Ile Ala Arg Asp Ala Arg
 260 265 270

Thr Ala Cys Glu Trp Gln Ser Phe Val Asn Asn Gln Ser Lys Leu Val
 275 280 285

Ser Asp Phe Gln Phe Ile Phe Leu Ala Leu Thr Gln Leu Gly Gln Asp
 290 295 300

Pro Asp Ala Met Thr Asp Cys Ser Ala Val Ile Pro Ile Ser Lys Pro
 305 310 315 320

Ala Pro Asn Asn Thr Pro Gly Phe Ser Phe Phe Pro Pro Gly Met Thr
 325 330 335

Met Asp Asp Val Glu Gln Ala Cys Ala Glu Thr Pro Phe Pro Thr Leu
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Ser Thr Leu Pro Gly Pro Ala Thr Ser Val Ala Arg Ile Pro Pro Pro
 355 360 365

Pro Gly Ala
 370

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 <211> 360
 <212> DNA
 <213> Solanum tuberosum

<400> 15

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 taataactaa ttatctgaat aagagaaaga gagatcatcc atatttctta tcctaaatga 180
 atgacagtgt ctttataatt ctttgatgaa cagatgcatt ttattaacca attccatata 240
 catataaata ttaatcatat ataattaata tcaattgggt agcaaaaccc aaatctagtc 300
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<210> 16
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 <212> DNA
 <213> Agrobacterium tumefaciens

<220>
 <221> CDS
 <222> (585)..(1826)
 <223> nopaline synthetase

<400> 16

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 aaccctgtgg ttggcatgca catacaaatg gacgaacgga taaacctttt cagccccttt 180
 taaatatccg ttattctaata aaacgctctt ttctcttagg tttaccgccc aatataatcct 240
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 agctagcaaa tatttcttgt caaaaatgct ccaactgacgt tccataaatt cccctcggta 540
 tccaattaga gtctcatatt cactctcaat ccaaataatc tgca atg gca att acc 596
 Met Ala Ile Thr

tta tcc gca act tct tta cct att tcc gcc gca gat cac cat ccg ctt Leu Ser Ala Thr Ser Leu Pro Ile Ser Ala Ala Asp His His Pro Leu 5 10 15 20	644
ccc ttg acc gta ggt gtc ctc ggt tct ggt cac gcg ggg act gca tta Pro Leu Thr Val Gly Val Leu Gly Ser Gly His Ala Gly Thr Ala Leu 25 30 35	692
gcg gct tgg ttc gcc tcc cgg cat gtt ccc acg gcg ctg tgg gca cca Ala Ala Trp Phe Ala Ser Arg His Val Pro Thr Ala Leu Trp Ala Pro 40 45 50	740
gca gat cat cca gga tcg atc tca gca atc aag gcc aat gaa gga gtt Ala Asp His Pro Gly Ser Ile Ser Ala Ile Lys Ala Asn Glu Gly Val 55 60 65	788
atc acc acc gag gga atg att aac ggt cca ttt agg gtc tca gcc tgt Ile Thr Thr Glu Gly Met Ile Asn Gly Pro Phe Arg Val Ser Ala Cys 70 75 80	836
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acc cgt gcg gac gtt cac gac agc ttc gtc aac gaa ctc gcc aac ttc Thr Arg Ala Asp Val His Asp Ser Phe Val Asn Glu Leu Ala Asn Phe 105 110 115	932
aac ggc gaa ctc gca aca aag gat att gtc gtc gtg tgc ggc cat ggc Asn Gly Glu Leu Ala Thr Lys Asp Ile Val Val Val Cys Gly His Gly 120 125 130	980
ttc tcc atc aag tac gag aga cag ctg cga ttc aag cga ata ttc gag Phe Ser Ile Lys Tyr Glu Arg Gln Leu Arg Phe Lys Arg Ile Phe Glu 135 140 145	1028
acg gat aat tcg ccc ata acg tct aag cta tcg gat caa aaa aaa tgt Thr Asp Asn Ser Pro Ile Thr Ser Lys Leu Ser Asp Gln Lys Lys Cys 150 155 160	1076
aac gtc aac atc aag gaa atg aaa gcg tct ttc gga ctg tca tgt ttc Asn Val Asn Ile Lys Glu Met Lys Ala Ser Phe Gly Leu Ser Cys Phe 165 170 175 180	1124
cca att cat cgc gat gat gct ggc gtg att gat cta ccc gaa gat acc Pro Ile His Arg Asp Asp Ala Gly Val Ile Asp Leu Pro Glu Asp Thr 185 190 195	1172
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tgc aac gtc caa gag caa ata gac cac gaa cgc cgg aag gtt gcc gca Cys Asn Val Gln Glu Gln Ile Asp His Glu Arg Arg Lys Val Ala Ala 280 285 290				1460
gcg tgt gga ttg cgt ctc aat tct ctc ttg cag gaa tgc aat gat gaa Ala Cys Gly Leu Arg Leu Asn Ser Leu Leu Gln Glu Cys Asn Asp Glu 295 300 305				1508
tat gat act gac tat gaa act ttg agg gaa tac tgc cta gca ccg tca Tyr Asp Thr Asp Tyr Glu Thr Leu Arg Glu Tyr Cys Leu Ala Pro Ser 310 315 320				1556
cct cat aac gtg cat cat gca tgc cct gac aac atg gaa cat cgc tat Pro His Asn Val His His Ala Cys Pro Asp Asn Met Glu His Arg Tyr 325 330 335 340				1604
ttt tct gaa gaa tta tgc tcg ttg gag gat gtc gcg gca att gca gct Phe Ser Glu Glu Leu Cys Ser Leu Glu Asp Val Ala Ala Ile Ala Ala 345 350 355				1652
att gcc aac atc gaa cta ccc ctc acg cat gca ttc atc aat att att Ile Ala Asn Ile Glu Leu Pro Leu Thr His Ala Phe Ile Asn Ile Ile 360 365 370				1700
cat gcg ggg aaa ggc aag att aat cca act ggc aaa tca tcc agc gtg His Ala Gly Lys Gly Lys Ile Asn Pro Thr Gly Lys Ser Ser Ser Val 375 380 385				1748
att ggt aac ttc agt tcc agc gac ttg att cgt ttt ggt gct acc cac Ile Gly Asn Phe Ser Ser Ser Asp Leu Ile Arg Phe Gly Ala Thr His 390 395 400				1796
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gatcgttcaa acatttggca ataaagtttc ttaagattga atcctgttgc cggtcttgcg				1906
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2521

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<213> Agrobacterium tumefaciens

<400> 17

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His His Pro Leu Pro Leu Thr Val Gly Val Leu Gly Ser Gly His Ala
20 25 30

Gly Thr Ala Leu Ala Ala Trp Phe Ala Ser Arg His Val Pro Thr Ala
35 40 45

Leu Trp Ala Pro Ala Asp His Pro Gly Ser Ile Ser Ala Ile Lys Ala
50 55 60

Asn Glu Gly Val Ile Thr Thr Glu Gly Met Ile Asn Gly Pro Phe Arg
65 70 75 80

Val Ser Ala Cys Asp Asp Leu Ala Ala Val Ile Arg Ser Ser Arg Val
85 90 95

Leu Ile Ile Val Thr Arg Ala Asp Val His Asp Ser Phe Val Asn Glu
100 105 110

Leu Ala Asn Phe Asn Gly Glu Leu Ala Thr Lys Asp Ile Val Val Val
115 120 125

Cys Gly His Gly Phe Ser Ile Lys Tyr Glu Arg Gln Leu Arg Phe Lys
130 135 140

Arg Ile Phe Glu Thr Asp Asn Ser Pro Ile Thr Ser Lys Leu Ser Asp
145 150 155 160

Gln Lys Lys Cys Asn Val Asn Ile Lys Glu Met Lys Ala Ser Phe Gly
165 170 175

Leu Ser Cys Phe Pro Ile His Arg Asp Asp Ala Gly Val Ile Asp Leu
180 185 190

Pro Glu Asp Thr Lys Asn Ile Phe Ala Gln Leu Phe Ser Ala Arg Ile
195 200 205

Ile Cys Ile Pro Pro Leu Gln Val Leu Phe Phe Ser Asn Cys Ile Thr
210 215 220

His Ala Val Pro Ala Val Met Asn Ile Gly Arg Leu Arg Asp Pro Ala
225 230 235 240

Asn Ser Leu Thr Lys Arg Ala Glu Lys Trp Leu Leu Glu Leu Asp Glu
245 250 255

Arg Thr Pro Arg Ala Glu Lys Gly Phe Phe Phe Tyr Gly Glu Gly Ser
260 265 270

Asn Thr Tyr Val Cys Asn Val Gln Glu Gln Ile Asp His Glu Arg Arg
275 280 285

Lys Val Ala Ala Ala Cys Gly Leu Arg Leu Asn Ser Leu Leu Gln Glu
290 295 300

Cys Asn Asp Glu Tyr Asp Thr Asp Tyr Glu Thr Leu Arg Glu Tyr Cys
305 310 315 320

Leu Ala Pro Ser Pro His Asn Val His His Ala Cys Pro Asp Asn Met
325 330 335

Glu His Arg Tyr Phe Ser Glu Glu Leu Cys Ser Leu Glu Asp Val Ala
340 345 350

Ala Ile Ala Ala Ile Ala Asn Ile Glu Leu Pro Leu Thr His Ala Phe
355 360 365

Ile Asn Ile Ile His Ala Gly Lys Gly Lys Ile Asn Pro Thr Gly Lys
370 375 380

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<210> 18

<211> 835

<212> DNA

<213> Streptomyces hygroscopicus

<400> 18

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gccgacatcc gccgtgccac cgaggcggac atgccggcgg tctgcaccat cgtcaaccac 240

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<223> PCR primer SP3R

<400> 22

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25